

E. Coli

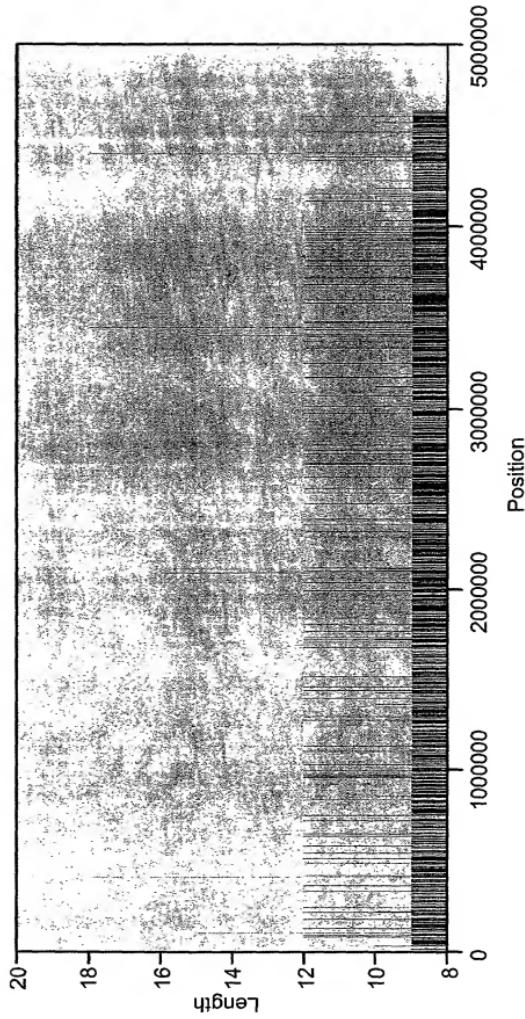


Fig. 1a

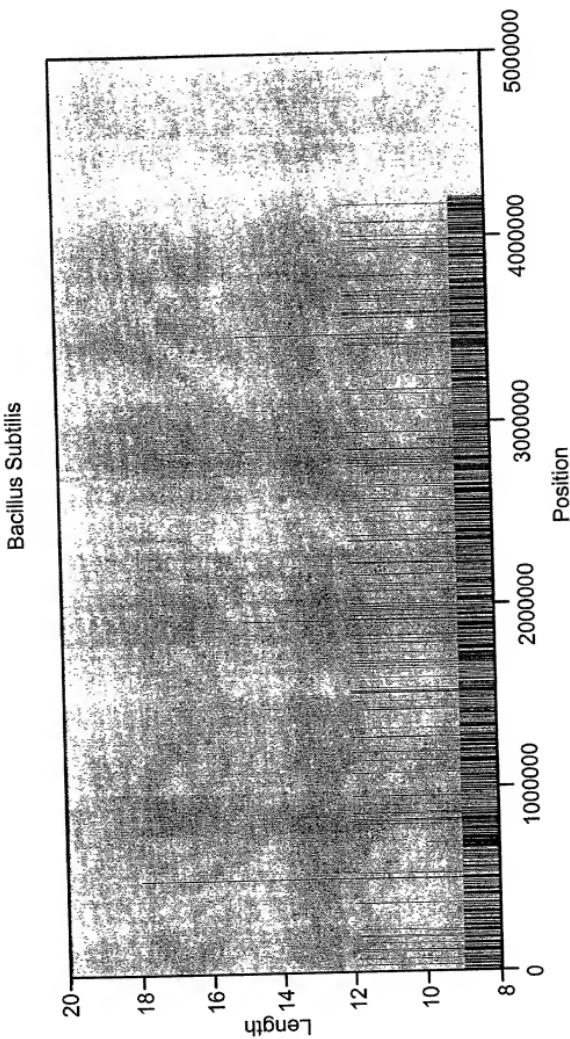


Fig. 1b

Archaeoglobus fulgidus

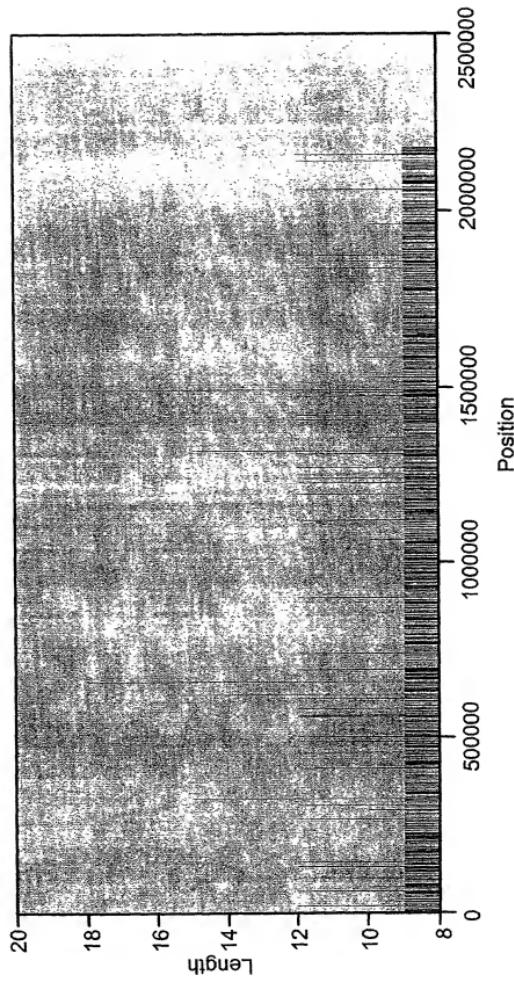


Fig. 1c

Yeast Chromosome 7

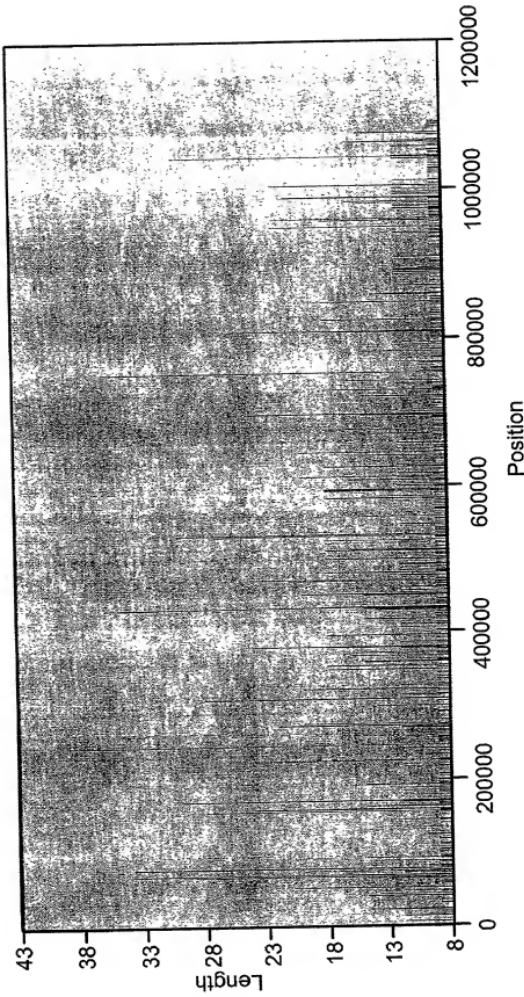


Fig. 1d

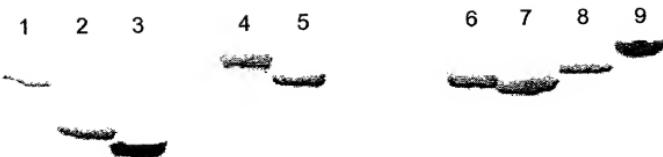


Fig. 2

		1	50
Ec K12, DH5a	---GTTATGT	CTTATCCAC	GTTATTTAAT ATGTTTCATT AGGATGTTA 25*
Ec Bsr9b	-TGTATGT	CTTATCCAC	GTTATTTAAT ATAGTTTCATT TGGATGTTCA 26*
Ec Bsr9c	TTGTTATGT	CTTATCCAC	GTTATTTAAT ATAGTTTCATT TGGATGTTCA 27*
Ec ETEC	-TCTATGTTC	TTATCNCAC	GTTTTTAAT ATGGTCATT AGGATGTTA 28*
Consensus	-----T-T--	-T---CCAC	GTTATTTAAT AT-GTTTCATT -GGATGTT-A 29*
	51	100	
Ec K12, DH5a	TTCTTGTATT	TTGCATATGA	GTATATTA.. CCCCCCCTC AAAAAATAA
Ec Bsr9b	TTCTTGTATT	TTGCATATGA	GTATATTA.. ...CCCTT CAAAAAATAA
Ec Bsr9c	TTCTTGTATT	TTGCATATGA	GTATATTA.. ...CCCTT CAAAAAATAA
Ec ETEC	TTCTTGTATT	TTGCATATGA	GTATATTAACC CCCCCCCTC AAAAAATAA
Consensus	TTCTT-ATT	TTGCATATGA	GTATATTA-- ---CCCT- -AAAAAATAA
	101	150	
Ec K12, DH5a	ATTAATTAAA	ATGATGGCTT	ATATAAAATA AAATTAAAG CAAGGAATCT
Ec Bsr9b	ATTAATTAAA	ACGATTGCTT	ATATAAAACA AAATTAAAG CAAGGAATCT
Ec Bsr9c	ATTAATTAAA	ACGATTGCTT	ATATAAAACA AAATTAAAG CAAGGAATCT
Ec ETEC	ATTAATTAAA	ATGATGGCTT	ATATAAAATA AAATTAAAG CAAGGAATCT
Consensus	ATTAATTAAA	A-GAT-GCTT	ATATAAA-A AAATTAAAG CAAGGAATCT
	151	200	
Ec K12, DH5a	CAATGGATGT	TAACACAAAT	GAGATTTGT GAAAGCAATA AATTATTGAC
Ec Bsr9b	CAATGGATGT	TAACACAAAT	GAGATTTGT GAAACACATA AATTATTGAC
Ec Bsr9c	CAATGGATGT	TAACACAAAT	GAGATTTGT GAAACACATA AATTATTGAC
Ec ETEC	CAATGGATGT	TAACACAAAT	GAGATTTGT GAANGCNATN NATTATTGNC
Consensus	CAATGGATGT	TAACACAAAT	GAGATTT-GT GAAA-CAATA AATTATT-AC
	201	250	
Ec K12, DH5a	TTGTTTTAG	ATTTGTTAG	CTATAATGTT ATACATTCAA ATGACTGAAC
Ec Bsr9b	TTGTTTTAG	ATTTGTTAG	CTATAATGTT ATACATTCAA ATGACTGAAC
Ec Bsr9c	TTGTTTTAG	ATTTGTTAG	CTATAATGTT ATACATTCAA ATGACTGAAC
Ec ETEC	TTGTTGTAN	ATTTGCTNAG	CTATAATGTT ATNCATTCAA ATGACTGAAC
Consensus	TTGTT-TAG	ATTTG-TTAG	CTATAATGTT ATACATTCAA ATGACTGAAC
	251	264	
Ec K12 DH5a	ATCCGTAAAT	TTAA	
Ec Bsr9b	ATCCGTAAAT	TAA-	
Ec Bsr9c	ATCCGTAAAT	TAA-	
Ec ETEC	ATCCGTNNT	TANA	
Consensus	ATCCGTAAAT	TAA-	

* SEQ ID NO

Fig. 3a

	1	50
Ec K12, DH5a	TTTNCGGAA AAAAATAGG AAAGGGGGG GGGCTAATCG	GCAGGGAAAGG 30*
Ec K12, w3110	TNTNNNCGG AAAAATATG AAAGGGGGGG GGGCTAATCG	GCAGGGAAAGG 31*
Ec Bsr9c	--TNTNCGG AAAAATATG AAA. GGGGG GGGCTAATCG	GCAGGGAAAGG 32*
Ec (wt) 1	--TNTNCGGAA AAAAANAGG AAAGGGGGGG GGGCTAATCG	GCAGGGAAAGG 33*
Ec (wt) 54	-----NCG GAAAAAAATG AAA. GGGGG GGGCTAATCG	GCAGGGAAAGG 34*
Ec (wt) 68	-----CG GAAAAAAATG AAA. GGGGG GGGCTAATCG	GCAGGGAAAGG 35*
Consensus	----- -AAAAAA--G AAA --GGGGG GGGCTAATCG	GCAGGGAAAGG 36*
	51	100
Ec K12, DH5a	CGCCCCCGGA TAGGGGGCGG CANAAGGAAT CANAATTTC	AGGTCAAGACG
Ec K12, w3110	CGCCCCCGGA TAGGGGGCGG CAGAAGGAAT CAGAATTTC	AGGTCAAGACG
Ec Bsr9c	CGCCCCCGGA TAGGGGGCGG CAGAAGGAAT CAGAATTTC	AGGTCAAGATG
Ec (wt) 1	CGCCCCCGGA TAGGGGGCGG CAGAAGGAAT CAGAATTTC	AGGTCAAGACG
Ec (wt) 54	CGCCCCCGGA TAGGGGGCGG CAGAAGGAAT CAGAATTTC	AGGTCAAGATG
Ec (wt) 68	CGCCCCCGGA TAGGGGGCGG CAGAAGGAAT CAGAATTTC	AGGTCAAGATG
Consensus	CGCCCCCGGA TAGGGGGCGG CAGAAGGAAT CAGAATTTC	AGGTCAAGACG
	101	150
Ec K12, DH5a	GGCTGCAAGT TGCAGACCGT TAAATCATC	GGNNNGGGTG TCGTACCCAC
Ec K12, w3110	GGCTGCAAGT TGCAGACCGT TAAATCATC	GGTTGGGGTG TCGTACCCAC
Ec Bsr9c	GGCTGCAAGT TGCAGACCGT TATAATCATC	GGTTGGGGTG TCGTACCCAC
Ec (wt) 1	GGCTGCAAGT TGCAGACCGT TAAATCATC	GGTTGGGGTG TCGTACCCAC
Ec (wt) 54	GGCTGCAAGT TGCAGACCGT TATAATCATC	GGTTGGGGTG TCGTACCCAC
Ec (wt) 68	GGCTGCAAGT TGCAGACCGT TATAATCATC	GGTTGGGGTG TCGTACCCAC
Consensus	GGCTGCAAGT TGCAGACCGT TA-AATCATC	GGTTGGGGTG TCGTACCCAC
	151	180
Ec K12, DH5a	CTTTACCTGC CGTCAGCCCC AGATTA- GTT -G	
Ec K12, w3110	CTTTACCTGC CGTCAGCCCC AGATTA- GTT -G	
Ec Bsr9c	CTTTACCTGC CGTCAGCCCC AGATTA- GTT -G	
Ec (wt) 1	CTTTACCTGC CGTCAGCCCC AGATTA- AA GTG TGG	
Ec (wt) 54	CTTTACCTGC CGTCAGCCCC AGAT- AA GTG TGG	
Ec (wt) 68	CTTTACCTGC CGTCAGCCCC AGAT- AA GTG TGG	
Consensus	CTTTACCTGC CGTCAGCCCC AGAT- AA GTG -G	

* SEQ ID NO

Fig. 3b

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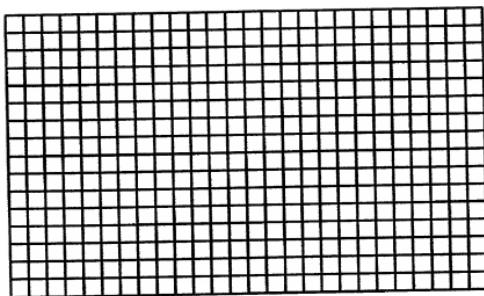


Fig. 4